



Blast 2 Sequences results

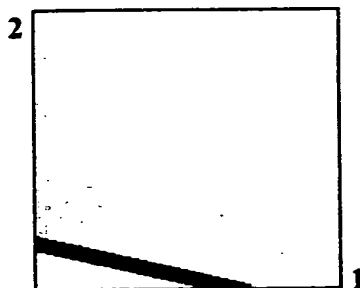
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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Nov-13-2000]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 137 (1 .. 137)

Sequence 2 lcl|seq_2 Length 569 (1 .. 569)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 167 bits (87), Expect = 8e-40

Identities = 93/96 (96%)

Strand = Plus / Minus

Query: 1 ccggttaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagcaca 60
|||||
Sbjct: 96 ccggttaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagctca 37

Query: 61 gatctctagagctgtcctgtcgctgccaggattga 96
|||||
Sbjct: 36 gatctctagagctgtcctgtcgccgccaggattga 1

CPU time: 0.02 user secs. 0.04 sys. secs 0.06 total secs.

Gapped

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

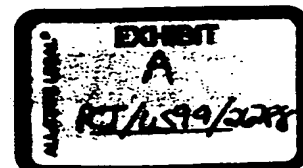
Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 1

Number of Sequences: 0

Number of extensions: 1

Number of successful extensions: 1



Number of sequenc better than 10.0: 1
length of query: 137
length of database: 2,635,864,967
effective HSP length: 22
effective length of query: 115
effective length of database: 2,635,864,945
effective search space: 303124468675
effective search space used: 303124468675
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)